

Substitute the paragraph beginning on page 55, line 23, with the following paragraph:

E5  
By "agonist" is intended naturally occurring and synthetic compounds capable of enhancing one or more activity of the ET2 and/or GABRE receptor subunit. Such agonists include modified forms of the ET2 or GABRE polypeptide and agents which increase expression of ET2 and/or GABRE receptor subunits. By "agonistic activity" is intended the enhancement of one or more ET2 and/or GABRE receptor subunit activities. By "antagonist" is intended naturally occurring and synthetic compounds capable of inhibiting one or more activities of the ET2 and/or GABRE receptor subunit. Such antagonists include modified forms of the ET2 or GABRE polypeptide and agents which decrease expression of ET2 and/or GABRE receptor subunits. By "antagonistic activity" is intended the inhibition of one or more ET2 and/or GABRE receptor subunit activities. Whether any candidate "agonist" or "antagonist" of the present invention can enhance or inhibit ET2 and/or GABRE receptor subunit activity can be determined using art-known assays, including those described in more detail below.

*In the Claims:*

Please substitute the following claims 95, 98, 101, 104, 115 and 117 for the pending claims 95, 98, 101, 104, 115 and 117:

E6  
Sub G1  
Sub 3  
95. (twice amended) An isolated polynucleotide comprising a nucleotide sequence encoding an amino acid sequence at least 95% identical to amino acids 1 to 260 of SEQ ID NO:42;

E6  
Cont

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids 1 to 260 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids 1 to 260 of SEQ ID NO:42.

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E7

Sub G2 ~~Sub 98~~ (twice amended) The isolated polynucleotide of claim 95, wherein said amino acid sequence is at least 95% identical to amino acids 1 to 488 of SEQ ID NO:42;

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids 1 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids 1 to 488 of SEQ ID NO:42.

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Sub G3 ~~Sub 101~~ (twice amended) The isolated polynucleotide of claim 98, wherein said amino acid sequence is at least 95% identical to amino acids -17 to 488 of SEQ ID NO:42;

E8

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids -17 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids -17 to 488 of SEQ ID NO:42.

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Sub G4 ~~Sub 104~~ (twice amended) The isolated polynucleotide of claim 101, wherein said amino acid sequence is at least 95% identical to amino acids -18 to 488 of SEQ ID NO:42;

E9

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids -18 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids -18 to 488 of SEQ ID NO:42.

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*Sub G5* *Sub 15*

(twice amended) An isolated polynucleotide comprising a nucleotide sequence encoding an amino acid sequence at least 95% identical to the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642,

*E10*

wherein % identity is determined with parameters that calculate % identity over the full length of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of amino acid residues of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.

*Sub G6* *Sub 16*

(twice amended) The isolated polynucleotide of claim 115, wherein said amino acid sequence is at least 95% identical to the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642;

*E11*

wherein % identity is determined with parameters that calculate % identity over the full length of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of amino acid residues of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.